

SEQUENCE LISTING

<110> Curtis, Rory A. J.
 Silos-Santiago, Inmaculada

<120> 53010, A NOVEL HUMAN CARBOXYLESTERASE
 FAMILY MEMBER AND USES THEREOF

<130> 10448-122001

<150> 60/256,369

<151> 2000-12-18

<150> 60/279,508

<151> 2001-03-28

<160> 6

<170> FastSEQ for Windows Version 4.0

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<212> DNA

<213> Homo sapiens

<220>

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<222> (96)...(1838)

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tca tct gct tca caa tgg tgc ttt ttc ctg att ctc cag ccc ctg ttg      161
Ser Ser Ala Ser Gln Trp Cys Phe Phe Leu Ile Leu Gln Pro Leu Leu
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gga cac aga cag tgg gga aaa act ggg cct tct gct gaa ggg cca cag      209
Gly His Arg Gln Trp Gly Lys Thr Gly Pro Ser Ala Glu Gly Pro Gln
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agg aac acc agg ctg gga tgg att cag ggc aag caa gtc act gtg ctg      257
Arg Asn Thr Arg Leu Gly Trp Ile Gln Gly Lys Gln Val Thr Val Leu
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Gly Ser Pro Val Pro Val Asn Val Phe Leu Gly Val Pro Phe Ala Ala
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ccc ccg ctg gga tcc ctg cga ttt acg aac ccg cag cct gca tcg ccc      353
Pro Pro Leu Gly Ser Leu Arg Phe Thr Asn Pro Gln Pro Ala Ser Pro
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aac tca gag tgg ctg ctc tta gat caa cac atg ctc aag gtg cat tac	449
Asn Ser Glu Trp Leu Leu Leu Asp Gln His Met Leu Lys Val His Tyr	
105 110 115	
ccg aaa ttc gga gtg tca gaa gac tgc ctc tac ctg aac atc tat gcg	497
Pro Lys Phe Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Ala	
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Pro Ala His Ala Asp Thr Gly Ser Lys Leu Pro Val Leu Val Trp Phe	
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cca gga ggt gcc ttc aag act ggc tca gcc tcc atc ttt gat ggg tcc	593
Pro Gly Gly Ala Phe Lys Thr Gly Ser Ala Ser Ile Phe Asp Gly Ser	
155 160 165	
gcc ctg gct gcc tat gag gac gtg ctg gtt gtg gtc gtc cag tac cgg	641
Ala Leu Ala Ala Tyr Glu Asp Val Leu Val Val Val Val Gln Tyr Arg	
170 175 180	
cta gga ata ttt ggt ttc ttc acc aca tgg gat cag cat gct ccg ggg	689
Leu Gly Ile Phe Gly Phe Phe Thr Thr Trp Asp Gln His Ala Pro Gly	
185 190 195	
aac tgg gcc ttc aag gac cag gtg gct gct ctg tcc tgg gtc cag aag	737
Asn Trp Ala Phe Lys Asp Gln Val Ala Ala Leu Ser Trp Val Gln Lys	
200 205 210	
aac atc gag ttc ttc ggt ggg gac ccc agc tct gtg acc atc ttt ggc	785
Asn Ile Glu Phe Phe Gly Gly Asp Pro Ser Ser Val Thr Ile Phe Gly	
215 220 225 230	
gag tcc gcg gga gcc ata agt gtt tct agt ctt ata ctg tct ccc atg	833
Glu Ser Ala Gly Ala Ile Ser Val Ser Ser Leu Ile Leu Ser Pro Met	
235 240 245	
gcc aaa ggc tta ttc cac aaa gcc atc atg gag agt ggg gtg gcc atc	881
Ala Lys Gly Leu Phe His Lys Ala Ile Met Glu Ser Gly Val Ala Ile	
250 255 260	
atc cct tac ctg gag gcc cat gat tat gag aag agt gag gac ctg cag	929
Ile Pro Tyr Leu Glu Ala His Asp Tyr Glu Lys Ser Glu Asp Leu Gln	
265 270 275	
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Val Val Ala His Phe Cys Gly Asn Asn Ala Ser Asp Ser Glu Ala Leu	
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ctg agg tgc ctg agg aca aaa ccc tcc aag gag ctg ctg acc ctc agc	1025
Leu Arg Cys Leu Arg Thr Lys Pro Ser Lys Glu Leu Leu Thr Leu Ser	
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cag aga ctc aaa gaa ccg cgg gtg gat ttt tgg acc agc acc atc ccc	1745

Gln Arg Leu Lys Glu Pro Arg Val Asp Phe Trp Thr Ser Thr Ile Pro
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ctg atc ctg tct gcc tcc gac atg ctc cac agt cct ctt tct tcc tta 1793
 Leu Ile Leu Ser Ala Ser Asp Met Leu His Ser Pro Leu Ser Ser Leu
 555 560 565

act ttc ctc tct ctc ctc cag cct ttc ttt ttc ttt tgt gct cct 1838
 Thr Phe Leu Ser Leu Leu Gln Pro Phe Phe Phe Phe Cys Ala Pro
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 <213> Homo sapiens

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 Ser Ala Glu Gly Pro Gln Arg Asn Thr Arg Leu Gly Trp Ile Gln Gly
 35 40 45
 Lys Gln Val Thr Val Leu Gly Ser Pro Val Pro Val Asn Val Phe Leu
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 Gly Val Pro Phe Ala Ala Pro Pro Leu Gly Ser Leu Arg Phe Thr Asn
 65 70 75 80
 Pro Gln Pro Ala Ser Pro Trp Asp Asn Leu Arg Glu Ala Thr Ser Tyr
 85 90 95
 Pro Asn Leu Cys Leu Gln Asn Ser Glu Trp Leu Leu Leu Asp Gln His
 100 105 110
 Met Leu Lys Val His Tyr Pro Lys Phe Gly Val Ser Glu Asp Cys Leu
 115 120 125
 Tyr Leu Asn Ile Tyr Ala Pro Ala His Ala Asp Thr Gly Ser Lys Leu
 130 135 140
 Pro Val Leu Val Trp Phe Pro Gly Gly Ala Phe Lys Thr Gly Ser Ala
 145 150 155 160
 Ser Ile Phe Asp Gly Ser Ala Leu Ala Ala Tyr Glu Asp Val Leu Val
 165 170 175
 Val Val Val Gln Tyr Arg Leu Gly Ile Phe Gly Phe Phe Thr Thr Trp
 180 185 190
 Asp Gln His Ala Pro Gly Asn Trp Ala Phe Lys Asp Gln Val Ala Ala
 195 200 205
 Leu Ser Trp Val Gln Lys Asn Ile Glu Phe Phe Gly Gly Asp Pro Ser
 210 215 220
 Ser Val Thr Ile Phe Gly Glu Ser Ala Gly Ala Ile Ser Val Ser Ser
 225 230 235 240
 Leu Ile Leu Ser Pro Met Ala Lys Gly Leu Phe His Lys Ala Ile Met
 245 250 255
 Glu Ser Gly Val Ala Ile Ile Pro Tyr Leu Glu Ala His Asp Tyr Glu

260 265 270
 Lys Ser Glu Asp Leu Gln Val Val Ala His Phe_Cys Gly Asn Asn Ala
 275 280 285
 Ser Asp Ser Glu Ala Leu Leu Arg Cys Leu Arg Thr Lys Pro Ser Lys
 290 295 300
 Glu Leu Leu Thr Leu Ser Gln Lys Thr Lys Ser Phe Thr Arg Val Val
 305 310 315 320
 Asp Gly Ala Phe Phe Pro Asn Glu Pro Leu Asp Leu Leu Ser Gln Lys
 325 330 335
 Ala Phe Lys Ala Ile Pro Ser Ile Ile Gly Val Asn Asn His Glu Cys
 340 345 350
 Gly Phe Leu Leu Pro Met Lys Glu Ala Pro Glu Ile Leu Ser Gly Ser
 355 360 365
 Asn Lys Ser Leu Ala Leu His Leu Ile Gln Asn Ile Leu His Ile Pro
 370 375 380
 Pro Gln Tyr Leu His Leu Val Ala Asn Glu Tyr Phe His Asp Lys His
 385 390 395 400
 Ser Leu Thr Glu Ile Arg Asp Ser Leu Leu Asp Leu Leu Gly Asp Val
 405 410 415
 Phe Phe Val Val Pro Ala Leu Ile Thr Ala Arg Tyr His Arg Asp Ala
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 Gly Ala Pro Val Tyr Phe Tyr Glu Phe Arg His Arg Pro Gln Cys Phe
 435 440 445
 Glu Asp Thr Lys Pro Ala Phe Val Lys Ala Asp His Ala Asp Glu Val
 450 455 460
 Arg Phe Val Phe Gly Gly Ala Phe Leu Lys Gly Asp Ile Val Met Phe
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 Glu Gly Ala Thr Glu Glu Lys Leu Leu Ser Arg Lys Met Met Lys
 485 490 495
 Tyr Trp Ala Thr Phe Ala Arg Thr Gly Asn Pro Asn Gly Asn Asp Leu
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 Ser Leu Trp Pro Ala Tyr Asn Leu Thr Glu Gln Tyr Leu Gln Leu Asp
 515 520 525
 Leu Asn Met Ser Leu Gly Gln Arg Leu Lys Glu Pro Arg Val Asp Phe
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 Trp Thr Ser Thr Ile Pro Leu Ile Leu Ser Ala Ser Asp Met Leu His
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<212> DNA

<213> Homo sapiens

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ttcggagtgt	cagaagactg	cctctacctg	aacatctatg	cgctgccc	cgccgataca	420
ggctccaagc	tccccgtctt	ggtgtggttc	ccaggaggtg	ccttcaagac	tggctcagcc	480
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<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence

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Leu Arg Phe Lys Ala Pro Gln Pro Tyr Lys Glu Pro Trp Ser Asp Val
 35          40          45
Leu Asp Ala Thr Lys Tyr Pro Pro Ser Cys Leu Gln Asp Asp Asp Phe
 50          55          60
Gly Phe Ser Leu Ser Asp Leu Lys Val Ala Leu Lys Met Leu Ser Leu
 65          70          75          80
Gly Trp Asn Lys Leu Val Gly Leu Lys Leu Ser Glu Asp Cys Leu Tyr
 85          90          95
Leu Asn Val Tyr Thr Pro Lys Asn Thr Lys Pro Asn Ser Lys Leu Pro
100          105          110
Val Met Val Trp Ile His Gly Gly Phe Met Phe Gly Ser Gly His
115          120          125
Ser Leu Pro Leu Ser Leu Tyr Asp Gly Glu Ser Leu Ala Arg Glu Gly
130          135          140
Asn Val Ile Val Val Ser Ile Asn Tyr Arg Leu Gly Pro Leu Gly Phe
145          150          155          160
Leu Ser Thr Gly Asp Asp Lys Leu Pro Gly Ser Gly Asn Tyr Gly Leu
165          170          175
Leu Asp Gln Arg Leu Ala Leu Lys Trp Val Gln Asp Asn Ile Ala Ala
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Phe Gly Gly Asp Pro Asn Ser Val Thr Ile Phe Gly Glu Ser Ala Gly
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Pro Ser Ser Lys Gly Leu Phe His Arg Ala Ile Ser Gln Ser Gly Ser
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245 250 255
Ala Lys Glu Leu Ala Arg Leu Leu Gly Cys Asn Glu Thr Ser Ser Ser
260 265 270
Glu Leu Leu Asp Cys Leu Arg Ser Lys Ser Ala Glu Glu Leu Leu Glu
275 280 285
Ala Thr Arg Ser Phe Leu Leu Phe Glu Tyr Val Pro Phe Leu Pro Leu
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Phe Leu Ala Phe Gly Pro Val Val Asp Gly Asp Asp Ala Pro Glu Ala
305 310 315 320
Phe Ile Pro Glu Asp Pro Glu Glu Leu Ile Lys Glu Gly Lys Phe Ala
325 330 335
Asp Val Pro Tyr Leu Ile Gly Val Thr Lys Asp Glu Gly Gly Tyr Phe
340 345 350
Ala Ala Met Leu Leu Asn Ala Ser Ser Lys Gly Glu Asp Glu Leu Lys
355 360 365
Lys Glu Thr Asn Pro Asp Val Trp Leu Glu Leu Leu Lys Tyr Leu Leu
370 375 380
Phe Tyr Ala Ser Glu Ala Leu Asn Ile Lys Asp Met Asp Asp Leu Ala
385 390 395 400
Asp Lys Val Leu Glu Lys Tyr Pro Gly Asp Val Asp Asp Phe Ser Val
405 410 415
Glu Ser Arg Lys Pro Asn Leu Gln Asp Met Leu Thr Asp Leu Leu Phe
420 425 430
Lys Cys Pro Thr Arg Val Ala Ala Asp Leu His Ala Lys His Gly Gly
435 440 445
Ser Pro Val Tyr Ala Tyr Val Phe Asp His Pro Ala Ser Phe Gly Ile
450 455 460
Gly Gln Phe Leu Ala Lys Arg Val Asp Pro Glu Phe Gly Gly Ala Val
465 470 475 480
His Gly Asp Glu Ile Phe Phe Val Phe Gly Asn Pro Leu Leu Lys Glu
485 490 495
Gln Leu Tyr Lys Ala Thr Glu Glu Glu Lys Ser Ser Ser Lys Thr
500 505 510
Met Met Asn Tyr Trp Ala Asn Phe Ala Lys Thr Gly Asn Pro Asn Asn
515 520 525
Gly Thr Ser Asn Gly Leu Val Val Trp Pro Lys Tyr Thr Ser Glu Glu
530 535 540
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<210> 5

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<212> PRT

<213> Artificial Sequence

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<223> Exemplary motif

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<223> Xaa = Gly, or Arg

<221> VARIANT

<222> 4-7, 9, 11, 13

<223> Xaa = Any amino acid

<221> VARIANT

<222> 8

<223> Xaa = Leu, Ile, Val, or Met

<221> VARIANT

<222> 10

<223> Xaa = Leu, Ile, or Val

<221> VARIANT

<222> 15

<223> Xaa = Ser, Thr, Ala, or Gly

<400> 5

Phe	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Ser	Xaa	Gly
1			5					10						15	

<210> 6

<211> 11

<212> PRT

<213> Artificial Sequence

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<223> Exemplary motif

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<223> Xaa = Glu, or Asp

<221> VARIANT

<222> 5

<223> Xaa = Tyr, or Thr

<221> VARIANT

<222> 6, 8

<223> Xaa = Leu, Ile, or Val

<221> VARIANT

<222> 7

<223> Xaa = Asp, Asn, or Ser

<221> VARIANT

<222> 9

<223> Xaa = Leu, Ile, Val, Phe, Tyr, or Trp

<221> VARIANT

<222> (0)...(10)

<223> Xaa = Any amino acid

<221> VARIANT

<222> (0)...(11)

<223> Xaa = Pro, Gln, or Arg

<400> 6

Xaa Asp Cys Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1

5

10

9

4

1

9